

PRINTER RUSH
(PTO ASSISTANCE)

Application : 09378759 Examiner : Beannock GAU : 1646
From: MPB Location: (IDC) FMF FDC Date: 10/18/05

Tracking #: QPM 09378759 Week Date: 05/02/05

DOC CODE	DOC DATE	MISCELLANEOUS
<input type="checkbox"/> 1449		<input type="checkbox"/> Continuing Data
<input type="checkbox"/> IDS		<input type="checkbox"/> Foreign Priority
<input type="checkbox"/> CLM		<input type="checkbox"/> Document Legibility
<input type="checkbox"/> IIFW		<input type="checkbox"/> Fees
<input type="checkbox"/> SRFW		<input type="checkbox"/> Other
<input checked="" type="checkbox"/> DRW	<u>02/19/03</u>	
<input type="checkbox"/> OATH		
<input type="checkbox"/> 312		
<input type="checkbox"/> SPEC		

ATTN: CHIEF DRAFTSPERSON OF THE OFFICE OF PATENT PUBLICATION

[RUSH] MESSAGE:

Ink "Tech center" stamp covers part of drawing sheets
(pages 4, 7, 10, 15, 22 and 23). Also, some of the figures
are illegible for capture. please provide replacement pages.

Thank you

[XRUSH] RESPONSE: SEE ATTACHMENTS

DRAWINGS CORRECTED

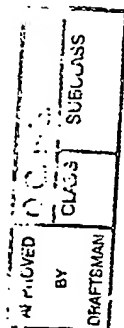
INITIALS: SZ

NOTE: This form will be included as part of the official USPTO record, with the Response document coded as XRUSH.
REV 10/04



FIG. 1D

CAG GTG ATC GGA GCA GGG GAG TTT GGC GAG GTC TGC AGT GGC CAC CTG Gln Val Ile Gly Ala Gly Glu Phe Gly Glu Val Cys Ser Gly His Leu 610 615 620	1872
AAG CTG CCA GGC AAG AGA GAG ATC TTT GTG GCC ATC AAG ACG CTC AAG Lys Leu Pro Gly Lys Arg Glu Ile Phe Val Ala Ile Lys Thr Leu Lys 625 630 635 640	1920
TCG GGC TAC ACG GAG AAG CAG CGC CGG GAC TTC CTG AGC GAA GCC TCC Ser Gly Tyr Thr Glu Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser 645 650 655	1968
ATC ATG GGC CAG TTC GAC CAT CCC AAC GTC ATC CAC CTG GAG GGT GTC Ile Met Gly Gln Phe Asp His Pro Asn Val Ile His Leu Glu Gly Val 660 665 670	2016
GTG ACC AAG AGC ACA CCT GTG ATG ATC ATC ACC GAG TTC ATG GAG AAT Val Thr Lys Ser Thr Pro Val Met Ile Ile Thr Glu Phe Met Glu Asn 675 680 685	2064
GGC TCC CTG GAC TCC TTT CTC CGG CAA AAC GAT GGG CAG TTC ACA GTC Gly Ser Leu Asp Ser Phe Leu Arg Gln Asn Asp Gly Gln Phe Thr Val 690 695 700	2112
ATC CAG CTG GTG GGC ATG CTT CGG GGC ATC GCA GCT GGC ATG AAG TAC Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr 705 710 715 720	2160
CTG GCA GAC ATG AAC TAT GTT CAC CGT GAC CTG GCT GCC CGC AAC ATC Leu Ala Asp Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 725 730 735	2208
CTC GTC AAC AGC AAC CTG GTC TGC AAG GTG TCG GAC TTT GGG CTC TCA Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser 740 745 750	2256
CGC TTT CTA GAG GAC GAT ACC TCA GAC CCC ACC TAC ACC AGT GCC CTG Arg Phe Leu Glu Asp Asp Thr Ser Asp Pro Thr Tyr Thr Ser Ala Leu 755 760 765	2304
GGC GGA AAG TTC CCC ATC CGC TGG ACA GCC CCG GAA GCC ATC CAG TAC Gly Gly Lys Phe Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr 770 775 780	2352
CGG AAG TTC ACC TCG GCC AGT GAT GTG TGG AGC TAC GGC ATT GTC ATG Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met 785 790 795 800	2400
TGG GAG GTG ATG TCC TAT GGG GAG CGG CCC TAC TGG GAC ATG ACC AAC Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Thr Asn 805 810 815	2448





Title: ANTIBODIES TO EPH-LIKE RECEPTOR
TYROSINE KINASES

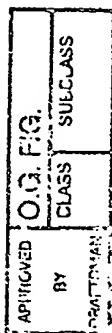
Inventors: FOX et al.

Application No.: 09/378,759

Attorney Docket No.: 6843.0027-03000

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FIG. 2B



TGC CCT TCT GTG GTA CGA CAC TTG GCT GTC TTC CCT GAC ACC ATC ACT	672
Cys Pro Ser Val Val Arg His Leu Ala Val Phe Pro Asp Thr Ile Thr	
210 215 220	
GGA GCT GAT TCT TCC CAA TTG CTC GAA GTG TCG GGC TCC TGT GTC AAC	720
Gly Ala Asp Ser Ser Gln Leu Leu Glu Val Ser Gly Ser Cys Val Asn	
225 230 235 240	
CAT TCT GTG ACC GAT GAA CCT CCC AAA ATG CAC TGC AGC GCC GAA GGG	768
His Ser Val Thr Asp Glu Pro Pro Lys Met His Cys Ser Ala Glu Gly	
245 250 255	
GAG TGG CTG GTG CCC ATC GGG AAA TGC ATG TGC AAG GCA GGA TAT GAA	816
Glu Trp Leu Val Pro Ile Gly Lys Cys Met Cys Lys Ala Gly Tyr Glu	
260 265 270	
GAG AAA AAT GGC ACC TGT CAA GTG TGC AGA CCT GGG TTC TTC AAA GCC	864
Glu Lys Asn Gly Thr Cys Gln Val Cys Arg Pro Gly Phe Phe Lys Ala	
275 280 285	
TCA CCT CAC ATC CAG AGC TGC GGC AAA TGT CCA CCT CAC AGT TAT ACC	912
Ser Pro His Ile Gln Ser Cys Gly Lys Cys Pro Pro His Ser Tyr Thr	
290 295 300	
CAT GAG GAA GCT TCA ACC TCT TGT GTC TGT GAA AAG GAT TAT TTC AGG	960
His Glu Glu Ala Ser Thr Ser Cys Val Cys Glu Lys Asp Tyr Phe Arg	
305 310 315 320	
AGA GAG TCT GAT CCA CCC ACA ATG GCA TGC ACA AGA CCC CCC TCT GCT	1008
Arg Glu Ser Asp Pro Pro Thr Met Ala Cys Thr Arg Pro Pro Ser Ala	
325 330 335	
CCT CGG AAT GCC ATC TCA AAT GTT AAT GAA ACT AGT GTC TTT CTG GAA	1056
Pro Arg Asn Ala Ile Ser Asn Val Asn Glu Thr Ser Val Phe Leu Glu	
340 345 350	
TGG ATT CCG CCT GCT GAC ACT GGT GGA AGG AAA GAC GTG TCA TAT TAT	1104
Trp Ile Pro Pro Ala Asp Thr Gly Gly Arg Lys Asp Val Ser Tyr Tyr	
355 360 365	
ATT GCA TGC AAG AAG TGC AAC TCC CAT GCA GGT GTG TGT GAG GAG TGT	1152
Ile Ala Cys Lys Lys Cys Asn Ser His Ala Gly Val Cys Glu Glu Cys	
370 375 380	
GGC GGT CAT GTC AGG TAC CTT CCC CGG CAA AGC GGC CTG AAA AAC ACC	1200
Gly Gly His Val Arg Tyr Leu Pro Arg Gln Ser Gly Leu Lys Asn Thr	
385 390 395 400	
TCT GTC ATG ATG GTG GAT CTA CTC GCT CAC ACA AAC TAT ACC TTT GAG	1248
Ser Val Met Met Val Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu	
405 410 415	



FIG. 2E

TAC TGG GAG ATG ACC AAT CAA GAT GTG ATT AAA GCG GTA GAG GAA GGC	2544
Tyr Trp Glu Met Thr Asn Gln Asp Val Ile Lys Ala Val Glu Glu Gly	
835 840 845	
TAT CGT CTG CCA AGC CCC ATG GAT TGT CCT GCT GCT CTC TAT CAG TTA	2592
Tyr Arg Leu Pro Ser Pro Met Asp Cys Pro Ala Ala Leu Tyr Gln Leu	
850 855 860	
ATG CTG GAT TGC TGG CAG AAA GAG CGA AAT AGC AGG CCC AAG TTT GAT	2640
Met Leu Asp Cys Trp Gln Lys Glu Arg Asn Ser Arg Pro Lys Phe Asp	
865 870 875 880	
GAA ATA GTC AAC ATG TTG GAC AAG CTG ATA CGT AAC CCA AGT AGT CTG	2688
Glu Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Ser Ser Leu	
885 890 895	
AAG ACG CTG GTT AAT GCA TCC TGC AGA GTA TCT AAT TTA TTG GCA GAA	2736
Lys Thr Leu Val Asn Ala Ser Cys Arg Val Ser Asn Leu Leu Ala Glu	
900 905 910	
CAT AGC CCA CTA GGA TCT GGG GCC TAC AGA TCA GTA GGT GAA TGG CTA	2784
His Ser Pro Leu Gly Ser Gly Ala Tyr Arg Ser Val Gly Glu Trp Leu	
915 920 925	
GAG GCA ATC AAG ATG GGC CGG TAT ACA GAG ATT TTC ATG GAA AAT GGA	2832
Glu Ala Ile Lys Met Gly Arg Tyr Thr Glu Ile Phe Met Glu Asn Gly	
930 935 940	
TAC AGT TCA ATG GAC GCT GTG GCT CAG GTG ACC TTG GAG GAT TTG AGA	2880
Tyr Ser Ser Met Asp Ala Val Ala Gln Val Thr Leu Glu Asp Leu Arg	
945 950 955 960	
CGG CTT GGA GTG ACT CTT GTC GGT CAC CAG AAG AAG ATC ATG AAC AGC	2928
Arg Leu Gly Val Thr Leu Val Gly His Gln Lys Lys Ile Met Asn Ser	
965 970 975	
CTT CAA GAA ATG AAG GTG CAG CTG GTA AAC GGA ATG GTG CCA TTG TAACTTCATG	2983
Leu Gln Glu Met Lys Val Gln Leu Val Asn Gly Met Val Pro Leu	
980 985 990	
TAAATGTCGC TTCCTCAAGT GAATGATTCT GCACTTTGTA AACAGCACTG AGATTTATTT	3043
TAACAAAAAA AGGGGGAAAA GGGAAAACAG TGATTTCTAA ACCTTAGAAA ACATTTGCCT	3103
CAGCCACAGA ATTTGTAATC ATGGTTTTAC TGAAGTATCC AGTTCTTAGT CCTTAGTCT	3162

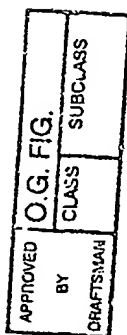
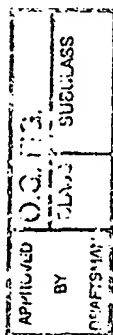




FIG. 3E

TGG AGC TAT GGA ATC GTT ATG TGG GAA GTG ATG TCG TAC GGG GAG AGG Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg 810 815 820	2502
CCC TAT TGG GAT ATG TCC AAT CAA GAT GTG ATT AAA GCC ATT GAG GAA Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu 825 830 835	2550
GGC TAT CGG TTA CCC CCT CCA ATG GAC TGC CCC ATT GCG CTC CAC CAG Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ile Ala Leu His Gln 840 845 850 855	2598
CTG ATG CTA GAC TGC TGG CAG AAG GAG AGG AGC GAC AGG CCT AAA TTT Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp Arg Pro Lys Phe 860 865 870	2646
GGG CAG ATT GTC AAC ATG TTG GAC AAA CTC ATC CGC AAC CCC AAC AGC Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Asn Ser 875 880 885	2694
TTG AAG AGG ACA GGG ACG GAG AGC TCC AGA CCT AAC ACT GCC TTG TTG Leu Lys Arg Thr Gly Thr Glu Ser Ser Arg Pro Asn Thr Ala Leu Leu 890 895 900	2742
GAT CCA AGC TCC CCT GAA TTC TCT GCT GTG GTA TCA GTG GGC GAT TGG Asp Pro Ser Ser Pro Glu Phe Ser Ala Val Val Ser Val Gly Asp Trp 905 910 915	2790
CTC CAG GCC ATT AAA ATG GAC CGG TAT AAG GAT AAC TTC ACA GCT GCT Leu Gln Ala Ile Lys Met Asp Arg Tyr Lys Asp Asn Phe Thr Ala Ala 920 925 930 935	2838
GGT TAT ACC ACA CTA GAG GCT GTG GTG CAC GTG AAC CAG GAG GAC CTG Gly Tyr Thr Thr Leu Glu Ala Val Val His Val Asn Gln Glu Asp Leu 940 945 950	2886
GCA AGA ATT GGT ATC ACA GCC ATC ACG CAC CAG AAT AAG ATT TTG AGC Ala Arg Ile Gly Ile Thr Ala Ile Thr His Gln Asn Lys Ile Leu Ser 955 960 965	2934
AGT GTC CAG GCA ATG CGA ACC CAA ATG CAG CAG ATG CAC GGC AGA ATG Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln Met His Gly Arg Met 970 975 980	2982
GTT CCC GTC TGAGCCAGTA CTGAATAAAC TCAAACTCT TGAAATTAGT Val Pro Val 985	3031
TTACCTCATC CATGCACTTT AATGAAGAA CTGCACTTTT TTTACTTCGT CTTCCGCCCTC	3091
TGAAATTAAA GAAATGAAAA AAAAA	3116



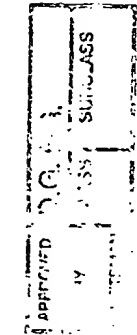


FIG. 5A

CONS MARARPP.....s..ll..llldal...aa.pa.Evtllldskt.qgelGwishPp..Gwee.sg.den.tprtYqCnvme.sqnn.WLrtnwi:
EPH MERRWPLGLGLVLLLCAPLPPGARAKEVTLMDSKAQGELGWLDPKDGWSEQQILNGT.PLYMYQDCPMQRRDTHWLRSNWIY
ECK MELQARACAFALLWGCALAAAAAQKEVLLDFAAAGGELGWLTHPYGKGWDLMONIMNDM.PIYMYSVCNVMSGDQDN.WLRTNWVY
HEK4 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWSYP SH.GWEEISGVDEHYTPRTYQVCNVMDHSQNN.WLRTNWVP
HEK5 LLAAVEETLMDSTTATAELGWMVHPPS.GWEEVSGYDENMNTIRTYQVCNVFESSQNN.WLRTKFIR
HEK7 ALRTLASPSNEVNLLDSRTVMGDLGWIAFPKN.GWEEIGEVDENYAPIHTYQVCCKVMEQNQNN.WLLTSWIS
HEK8 MAGIFYFALFSCFLGICDAVTGSRVYPANEVTLDSRSVQELGWIASPLEGGWEEVSIMDEKNTPIRTYQVCNVMEPSQNN.WLRTDWIT
HEK2 MARARPPPPPPGLLPLPLPLPLLLPAGCRALLETLMDTKWVTSELAWTSHPS.GWEEVSGYDEAMNPIRTYQVCNVRESSQNN.WLRTGFIW
HEK11 MVFQTRYP SWIILCYINLLRFAHTGEAQAAKEVLLLDLSKAQQTLEWISSPPN.GWEEISGLDENYTPRTYQVCQVMEPNQNN.WLRTNWIS
*
*
CONS rg.gaqrIyVelkft.RDCnS.Pgvlgt..CKETFNlyyEsddd....tgrniren.fvKiDtIAaDesftq.Dlgdr.mklnTevrsvGpLskkGfYL
EPH RGEASRVHVELQFTVRDCKSFPGAGPLGCKETFNLLYMESDQD....VGIQLRRPLFQKVTYVAADQSFTIRDLASGSVKLNVERCSLGRLTRGLYL
ECK RG.EAERNNFELNFTVRDCNSFPFGASS..CKETFNLYYAESDLD....YGTNFQKRLFTKIDTIAPDEITVSSDFEARHVKLNVEERSVGPLTRKGFYL
HEK4 RN.SAQKIYVELKFTLRDCNSIPLVLGT..CKETFNLYYMESDDD....HG VKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYL
HEK5 RR.GAHRIHVEMKFSVRDCSSIPSVP GS..CKETFNLYYEAADFSA TKTFPNMNMENPVKVD TIAADESFSQVDLGGRVNKNINTEVRSFGPVSRS GFYL
HEK7 NE.GASRIFIELKFTLRDCNSLPGGLGT..CKETFNMYEFESDDQ....NGRNKENQYIKIDTIAADESFTELDGLDRVMLNTEVRDVGPLSKKGFYL
HEK8 RE.GAQRVYIEIKFTLRDCNSLPGVMGT..CKETFNLYYYESDND....KERFIRENQFVKIDTIAADESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYL
HEK2 RR.DVQRVYVELKFTVRDCNSIPNIPGS..CKETFNLFYVYEA DSDVASASSPFWMENPVKVD TIADESFSRLDAGR V...NTKVR SFGLPSKAGFYL
HEK11 KG.NAQRIFVELKFTLRDCNSLPGVLGT..CKETFNLYYETDYD....TGRNIRENLYVKIDTIAADESFTQGDIGERKMLNTEVREIGPLSQKGFYL



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